

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/530,217  
Source: PCT  
Date Processed by STIC: 4-12-05

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PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/530,217

DATE: 04/12/2005

TIME: 14:05:35

Input Set : A:\082368-003910US.txt

Output Set: N:\CRF4\04122005\J530217.raw

```

4 <110> APPLICANT: Nakamura, Yusuke
5           Katagiri, Toyomasa
7 <120> TITLE OF INVENTION: GENES AND POLYPEPTIDES RELATING TO HUMAN
8           MYELOID LEUKEMIA
10 <130> FILE REFERENCE: 082368-003910US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/530,217
C--> 12 <141> CURRENT FILING DATE: 2005-03-30
12 <150> PRIOR APPLICATION NUMBER: PCT/JP03/09589
13 <151> PRIOR FILING DATE: 2003-07-29
15 <150> PRIOR APPLICATION NUMBER: US 60/414,867
16 <151> PRIOR FILING DATE: 2002-09-30
18 <160> NUMBER OF SEQ ID NOS: 16
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 22
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
29           RT-PCR
31 <400> SEQUENCE: 1
32 gtgctttcc tcttcaccc tt          22
34 <210> SEQ ID NO: 2
35 <211> LENGTH: 23
36 <212> TYPE: DNA
37 <213> ORGANISM: Artificial Sequence
39 <220> FEATURE:
40 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
41           RT-PCR
44 <400> SEQUENCE: 2
45 ggtggtcgtc aagaaaacaag tta      23
47 <210> SEQ ID NO: 3
48 <211> LENGTH: 23
49 <212> TYPE: DNA
50 <213> ORGANISM: Artificial Sequence
52 <220> FEATURE:
53 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
54           RT-PCR
56 <400> SEQUENCE: 3
57 catccacgaa actaacccca act          23
59 <210> SEQ ID NO: 4
60 <211> LENGTH: 23
61 <212> TYPE: DNA

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62 <213> ORGANISM: Artificial Sequence  
64 <220> FEATURE:  
65 <223> OTHER INFORMATION: Artificially synthesized primer sequence for  
66 RT-PCR  
68 <400> SEQUENCE: 4  
69 tcccttaga gagaagtggg gtg 23  
71 <210> SEQ ID NO: 5  
72 <211> LENGTH: 22  
73 <212> TYPE: DNA  
74 <213> ORGANISM: Artificial Sequence  
76 <220> FEATURE:  
77 <223> OTHER INFORMATION: Artificially synthesized primer sequence for  
78 RT-PCR  
80 <400> SEQUENCE: 5  
81 gtgtcttcc tcttcacatt tg 22  
83 <210> SEQ ID NO: 6  
84 <211> LENGTH: 23  
85 <212> TYPE: DNA  
86 <213> ORGANISM: Artificial Sequence  
88 <220> FEATURE:  
89 <223> OTHER INFORMATION: Artificially synthesized primer sequence for  
90 RT-PCR  
92 <400> SEQUENCE: 6  
93 ggtggtcgtc aagaaacaag tta 23  
95 <210> SEQ ID NO: 7  
96 <211> LENGTH: 23  
97 <212> TYPE: DNA  
98 <213> ORGANISM: Artificial Sequence  
100 <220> FEATURE:  
101 <223> OTHER INFORMATION: Artificially synthesized primer sequence for  
102 RT-PCR  
104 <400> SEQUENCE: 7  
105 gacaactcac tcaaggattgt cag 23  
107 <210> SEQ ID NO: 8  
108 <211> LENGTH: 20  
109 <212> TYPE: DNA  
110 <213> ORGANISM: Artificial Sequence  
112 <220> FEATURE:  
113 <223> OTHER INFORMATION: Artificially synthesized primer sequence for  
115 RT-PCR  
117 <400> SEQUENCE: 8  
118 gatccacgac ggacacattg 20  
120 <210> SEQ ID NO: 9  
121 <211> LENGTH: 28  
122 <212> TYPE: DNA  
123 <213> ORGANISM: Artificial Sequence  
125 <220> FEATURE:  
126 <223> OTHER INFORMATION: Artificially synthesized primer sequence for  
127 RT-PCR

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129 <400> SEQUENCE: 9
130 cggaaattccg atgagtgagg cccgcagg 28
132 <210> SEQ ID NO: 10
133 <211> LENGTH: 29
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
137 <220> FEATURE:
138 <223> OTHER INFORMATION: Artificially synthesized primer sequence for
139 RT-PCR
141 <400> SEQUENCE: 10
142 ggggtacccc agtggagctg agcgtccag 29
144 <210> SEQ ID NO: 11
145 <211> LENGTH: 18
146 <212> TYPE: DNA
147 <213> ORGANISM: Artificial Sequence
149 <220> FEATURE:
150 <223> OTHER INFORMATION: Artificially synthesized S-oligonucleotide
151 sequence for antisense
153 <400> SEQUENCE: 11
154 ctgtgtgatg gacgtctg 18
156 <210> SEQ ID NO: 12
157 <211> LENGTH: 18
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: S-oligonucleotide sequence for antisense
164 <400> SEQUENCE: 12
165 gtctgcaggat agtgtgtc 18
167 <210> SEQ ID NO: 13
168 <211> LENGTH: 19
169 <212> TYPE: DNA
170 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: Target sequence for siRNA
175 <400> SEQUENCE: 13
176 gtacgtgcag caggagaac 19
178 <210> SEQ ID NO: 14
179 <211> LENGTH: 19
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Target sequence for siRNA
186 <400> SEQUENCE: 14
187 gaagcagcac gacttcttc 19
189 <210> SEQ ID NO: 15
190 <211> LENGTH: 2958
191 <212> TYPE: DNA
192 <213> ORGANISM: Homo sapiens
194 <220> FEATURE:

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195 <221> NAME/KEY: CDS
196 <222> LOCATION: (111)...(2678)
198 <400> SEQUENCE: 15
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200 ccccccagag acccccgccg gcggcagcct gccttgctct gccaggaacc atg agt 116
201 116
202 116
203 Met Ser
204 116
205 164
206 5 10 15
207 164
208 tgg cta aag ctg gac att ccc tct gcg gtg ccc ctg acg gca gaa gag 212
209 Trp Leu Lys Leu Asp Ile Pro Ser Ala Val Pro Leu Thr Ala Glu Glu
210 20 25 30
211 212
212 ccc agc ttc ctg cag ccc ctg agg cga cag gct ttc ctg agg agt gtg 260
213 Pro Ser Phe Leu Gln Pro Leu Arg Arg Gln Ala Phe Leu Arg Ser Val
214 35 40 45 50
215 260
216 agt atg cca gcc gag aca gcc cac atc tct tca ccc cac cat gag ctc 308
217 Ser Met Pro Ala Glu Thr Ala His Ile Ser Ser Pro His His Glu Leu
218 55 60 65
219 308
220 cgg cgg ccg gtg ctg caa cgc cag acg tcc atc aca cag acc atc cgc 356
221 Arg Arg Pro Val Leu Gln Arg Gln Thr Ser Ile Thr Gln Thr Ile Arg
222 70 75 80
223 356
224 agg ggg acc gcc gac tgg ttt gga gtg agc aag gac agt gac agc acc 404
225 Arg Gly Thr Ala Asp Trp Phe Gly Val Ser Lys Asp Ser Asp Ser Thr
226 85 90 95
227 404
228 cag aaa tgg cag cgc aag agc atc cgt cac tgc agc cag cgc tac ggg 452
229 Gln Lys Trp Gln Arg Lys Ser Ile Arg His Cys Ser Gln Arg Tyr Gly
230 100 105 110
231 452
232 aag ctg aag ccc cag gtc ctc cgg gag ctg gac ctg ccc agc cag gac 500
233 Lys Leu Lys Pro Gln Val Leu Arg Glu Leu Asp Leu Pro Ser Gln Asp
234 115 120 125 130
235 500
236 aac gtg tcg ctg acc agc acc gag acg cca ccc cca ctc tac gtg ggg 548
237 Asn Val Ser Leu Thr Ser Thr Glu Thr Pro Pro Leu Tyr Val Gly
238 135 140 145
239 548
240 cca tgc cag ctg ggc atg cag aag atc ata gac ccc ctg gcc cgt ggc 596
241 Pro Cys Gln Leu Gly Met Gln Lys Ile Ile Asp Pro Leu Ala Arg Gly
242 150 155 160
243 596
244 cgt gcc ttc cgt gtg gca gat gac act gcg gaa ggc ctg agt gcc cca 644
245 Arg Ala Phe Arg Val Ala Asp Asp Thr Ala Glu Gly Leu Ser Ala Pro
246 165 170 175
247 644
248 cac act ccc gtc acg ccg ggt gct gcc tcc ctc tgc tcc ttc tcc agc 692
249 His Thr Pro Val Thr Pro Gly Ala Ala Ser Leu Cys Ser Phe Ser Ser
250 180 185 190
251 692
252 tcc cgc tca ggt ttc cac ccg ctc ccg cgg cgg cgc aag cga gag tcg 740
253 Ser Arg Ser Gly Phe His Arg Leu Pro Arg Arg Arg Lys Arg Glu Ser
254 195 200 205 210
255 740
256 gtg gcc aag atg agc ttc ccg gcg gcc gca gcg ctg atg aaa ggc cgc 788
257 Val Ala Lys Met Ser Phe Arg Ala Ala Ala Leu Met Lys Gly Arg
258 210 220 225

```

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260	tcc	gtt	agg	gat	ggc	acc	ttt	cgc	cg	gca	cg	cgt	cga	agc	ttc	act	836
261	Ser	Val	Arg	Asp	Gly	Thr	Phe	Arg	Arg	Ala	Arg	Arg	Arg	Ser	Phe	Thr	
262																240	
263	230							235									
264	cca	gct	agc	ttt	ctg	gag	gag	gac	aca	act	gat	ttc	ccc	gat	gag	ctg	884
265	Pro	Ala	Ser	Phe	Leu	Glu	Glu	Asp	Thr	Thr	Asp	Phe	Pro	Asp	Glu	Leu	
266																	
267	245						250								255		
268	gac	aca	tcc	ttt	gcc	cg	gaa	ggt	atc	ctc	cat	gaa	gag	ctg	tcc	932	
269	Asp	Thr	Ser	Phe	Phe	Ala	Arg	Glu	Gly	Ile	Leu	His	Glu	Glu	Leu	Ser	
270																	
271	260						265								270		
272	aca	tac	ccg	gat	gaa	gtt	ttc	gag	tcc	cca	tcg	gag	gca	g	cta	aag	980
273	Thr	Tyr	Pro	Asp	Glu	Val	Phe	Glu	Ser	Pro	Ser	Glu	Ala	Ala	Leu	Lys	
274	275						280									290	
275	gac	tgg	gag	aag	gca	ccg	gag	cag	g	ctc	acc	ggc	ggg	gcc	ctg	1028	
276	Asp	Trp	Glu	Lys	Ala	Pro	Glu	Gln	Ala	Asp	Leu	Thr	Gly	Gly	Ala	Leu	
277																	
278	295						300								305		
279	gac	cg	ag	g	tt	g	g	cg	ag	c	ct	at	g	cc	tt	g	980
280	Asp	Arg	Ser	Glu	Leu	Glu	Arg	Ser	His	Leu	Met	Leu	Pro	Leu	Glu	Arg	
281																	
282	310						315								320		
283	ggc	tgg	cg	aag	cag	aag	gag	ggc	gca	g	cc	cag	ccc	aag	gt	1124	
284	Gly	Trp	Arg	Lys	Gln	Lys	Glu	Gly	Ala	Ala	Ala	Pro	Gln	Pro	Lys	Val	
285																	
286	325						330								335		
287	cg	ctc	cg	cag	gag	gt	gt	ag	acc	g	gg	gg	cg	gg	cag	1172	
288	Arg	Leu	Arg	Gln	Glu	Val	Val	Ser	Thr	Ala	Gly	Pro	Arg	Arg	Gly	Gln	
289																	
290	340						345								350		
291	cgt	atc	gc	gt	cg	gt	cg	cg	atc	ttc	g	cc	g	aa	cg	cc	1220
292	Arg	Ile	Ala	Val	Pro	Val	Arg	Lys	Leu	Phe	Ala	Arg	Glu	Lys	Arg	Pro	
293																	
294	355						360								370		
295	tat	ggg	ctg	ggc	atg	gt	gg	cg	ctc	acc	aa	cgc	acc	tac	cgc	aag	1268
296	Tyr	Gly	Leu	Gly	Met	Val	Gly	Arg	Leu	Thr	Asn	Arg	Thr	Tyr	Arg	Lys	
297																	
298	375						380								385		
299	cg	atc	gac	ag	ttc	gtc	aag	cg	cag	atc	gag	gac	atg	gac	gac	cac	1316
300	Arg	Ile	Asp	Ser	Phe	Val	Lys	Arg	Gln	Ile	Glu	Asp	Met	Asp	Asp	His	
301																	
302	390						395								400		
303	agg	ccc	ttc	ttc	acc	ta	c	tgg	ctt	acc	ttc	gt	cac	tc	gtc	acc	1364
304	Arg	Pro	Phe	Phe	Thr	Tyr	Trp	Leu	Thr	Phe	Val	His	Ser	Leu	Val	Thr	
305																	
306	405						410								415		
307	atc	cta	gc	gt	tg	atc	ta	ttc	gg	atc	g	cc	gt	gg	ttc	tcg	1412
308	Ile	Leu	Ala	Val	Cys	Ile	Tyr	Gly	Ile	Ala	Pro	Val	Gly	Phe	Ser	Gln	
309																	
310	420						425								430		
311	cat	gag	ac	gt	g	tc	gt	cg	aa	cgc	gg	gt	tc	g	aa	1460	
312	His	Glu	Thr	Val	Asp	Ser	Val	Leu	Arg	Asn	Arg	Gly	Val	Tyr	Glu	Asn	
313																	
314	435						440								450		
315	gt	aag	ta	gt	cg	ca	g	tg	at	gg	cc	ag	tc	g	aa	1508	
316	Val	Lys	Tyr	Val	Gln	Gln	Glu	Asn	Phe	Trp	Ile	Gly	Pro	Ser	Ser	Glu	
317																	
318	455						460								465		
319	gcc	ctc	atc	ca	ct	gg	gc	aag	ttt	tc	cc	tc	at	cg	ca	gc	1556
320	Ala	Leu	Ile	His	Leu	Gly	Ala	Lys	Phe	Ser	Pro	Cys	Met	Arg	Gln	Asp	
321																	
322	470						475								480		
323	ccg	cag	gt	ca	ag	ttc	at	cg	tc	gg	cg	cg	gag	cg	ca	cac	1604
324																	

**VERIFICATION SUMMARY**

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date